REPORT

ARS

CEREAL RUST

WORKSHOP

St. Louis, Missouri

May 24-25, 1994

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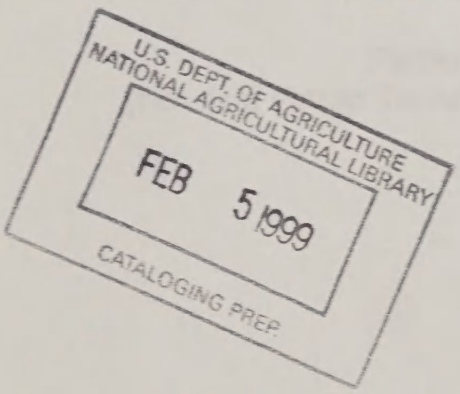
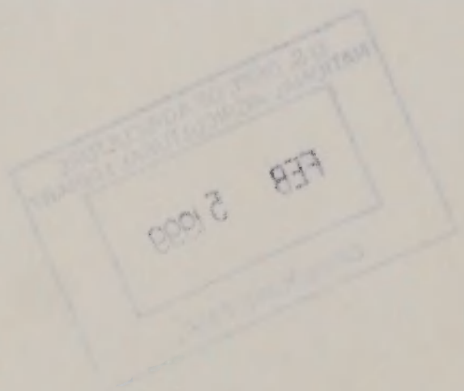




AGENDA

ARS Cereal Rust Workshop

St. Louis, Missouri

May 24-26, 1994

Welcome & Workshop Objectives	Chuck Murphy Roy Gingery
Introductions	Participants
Establish Disease-Host Priorities	Participants
Determine Research Needs	Participants (Nominal Group Technique)
Prioritize Research Needs	Participants (Nominal Group Technique)
Summary, Thoughts/Concerns	All

WORKSHOP OBJECTIVES

Cereal rusts, along with barley yellow dwarf virus, are the most serious disease threats to small grain production. ARS programs have, for many years, been a major part of the overall cereal rust research effort in the U.S. Budgetary constraints have resulted in an overall reduction in the number of cereal rust programs. Thus, ARS cereal rust research now represents a larger portion of a smaller total effort.

This workshop was convened to help ARS focus its available resources on those problems of greatest relevance. The invited participants brought a broad range of scientific expertise and perspectives to the workshop. Their willingness to share expertise, experience, and vision was essential to the fulfillment of the workshop objectives.

The order of business was:

- Introductions and overview of current ARS cereal rust research efforts.
- Prioritization of rust disease problems within each cereal crop (group consensus)
- Determination of research needs and prioritization for each host/disease combination (nominal group technique).

NOTE: Increasing occurrences of the toxin-producing scab disease pathogen and the possibility of addressing this problem at the Cereal Rust Laboratory prompted inclusion of this disease problem in the discussions and subsequent research needs assessment.

DISEASE/HOST PRIORITIES

The priority of rust disease problems within each host species was determined by consensus. These priorities were:

Wheat

1	-	Leaf Rust
2	-	Stem Rust
3	-	Stripe Rust

Oats

1	-	Crown Rust
2	-	Stem Rust

Barley

1	-	Stripe Rust
2-3	-	Leaf Rust
2-3	-	Stem Rust
4	-	Crown Rust

RESEARCH NEEDS IDENTIFICATION

A no-discussion, no-debate, "brainstorming" technique was utilized to elicit a listing of research needs from the group. The initial listing was then organized by the program leaders, presented to the full group and slightly modified into a listing as follows:

HOST

1. Germplasm Acquisition and Evaluation
    a. Evaluate diverse germplasm
    b. Search for resistant germplasm

2. Germplasm Enhancement
    a. Maintain near isogenic lines for rust resistance
    b. Breeding for resistance
    c. Improve breeding systems
    d. Create linkage block for durable resistance
    e. Extend durability of resistance
    f. Utilize genes for anti-fungal substances

3. Gene Mapping
    a. Develop transposon technology for small grains
    b. Map host genes for resistance
    c. Determine relationship between physical and genetic distances
    d. Determine distribution of resistance genes
    e. Tag genes with high heritability characteristics
    f. Determine relationship among resistance genes in different cereals
    g. Coordinate genome mapping across species
    h. Mark genes with low heritability characteristics
    i. Create large-insert genomic libraries

4. Cytology/Wide Crossing
    a. Develop improved methods for alien gene transfer
    b. Manipulate chromosomes efficiently
    c. Develop and maintain cytogenetic stocks

5. Mechanisms of Resistance
    a. Characterize defense response genes
    b. Elucidate molecular basis of non-host resistance
    c. Describe mechanisms of resistance and host-parasite interactions
    d. Determine the molecular basis of resistance
    e. Characterize pre-infection resistance responses
    f. Determine environmental effects

6. Genome Manipulation
    a. Develop efficient transformation techniques
    b. Develop resistance via mutation
    c. Transfer genes from other sources
    d. Clone resistance genes

7. Genetics
    a. Elucidate inheritance of slow rusting
    b. Identify resistance genes
    c. Determine interactions between homo- and heterozygous resistance genes
    d. Identify the effect of genetic background in resistance genes
    e. Determine gene action and interaction via classical genetics

PATHOGEN

8. Genome Mapping/Manipulation
    a. Create large-insert genomic libraries
    b. Develop genetic and physical maps of pathogenic fungi
    c. Develop transformation systems for fungal pathogens

9. Develop and Maintain Pathogen Germplasm
    a. Maintain long-term storage of rust isolates
    b. Develop strategy for rust germplasm collection and preservation
    c. Develop clearing house for tester strain distribution
    d. Develop tester pathogen strains with single avirulence genes

10. Fungal Population Genetics
    a. Determine geographic structure of rust populations
    b. Determine population dynamics of virulence
    c. Define effects of distribution of resistance genes on race dynamics

11. Fungal Genetics
    a. Elucidate specificity of forma specialis
    b. Determine gene action and interaction via classical genetics
    c. Describe genetics of pathogen
    d. Characterize avirulence and pathogenicity genes
    e. Describe genetics of fungal development

12. Evolution and Systematics
    a. Develop phylogenetic tree for rusts
    b. Create pathogen variants to anticipate race shifts
    c. Determine basis for genetic variability of virulence
    d. Determine effects of avirulence genes on rust fitness
    e. Describe fungal variability and evolution

13. Metabolism and Physiology
    a. Elucidate fungal metabolism
    b. Describe physiology of fungal infection
    c. Induce germination in dormant spores
    d. Manipulate fungal life cycle

DISEASE

14. Epidemiology/Monitoring/Prediction
    a. Improve spore detection methodology
    b. Monitor rust populations for new pathotypes
    c. Determine effectiveness of gene deployment strategies
    d. Determine non-crop inoculum sources
    e. Determine epidemiology yield-loss thresholds .
    f. Characterize survival of primary inoculum
    g. Describe the effect of pre-infection biology on disease
    h. Monitor rusts internationally
    i. Develop/improve rust forecasting systems
    j. Develop methods to quantify national rust losses

15. Chemical Control
    a. Develop, evaluate and utilize fungicidal controls
    b. Describe cytology and physiology of interactions
    c. Elucidate receptivity to infection

16. Screening Methodology (for Resistance)
    a. Develop an improved disease screening methodology
    b. Improve disease severity assessment methodology

17. Coordinate Regional/International Testing
    a. Revive international rust nursery
    b. Coordinate regional testing program

18. Biological Control
    a. Identify natural fungicides
    b. Develop biological control methods

19. Management Systems
    a. Develop expert systems for disease management
    b. Determine effect of management practices on disease
    c. Determine effects of minimum tillage on disease development
    d. Develop non-traditional control methods

20. Ecology
    a. Determine interactions among rusts and other pests
    b. Manipulate/describe the ecology of dormancy
    c. Identify effects of physical and biological factors on rust fungi

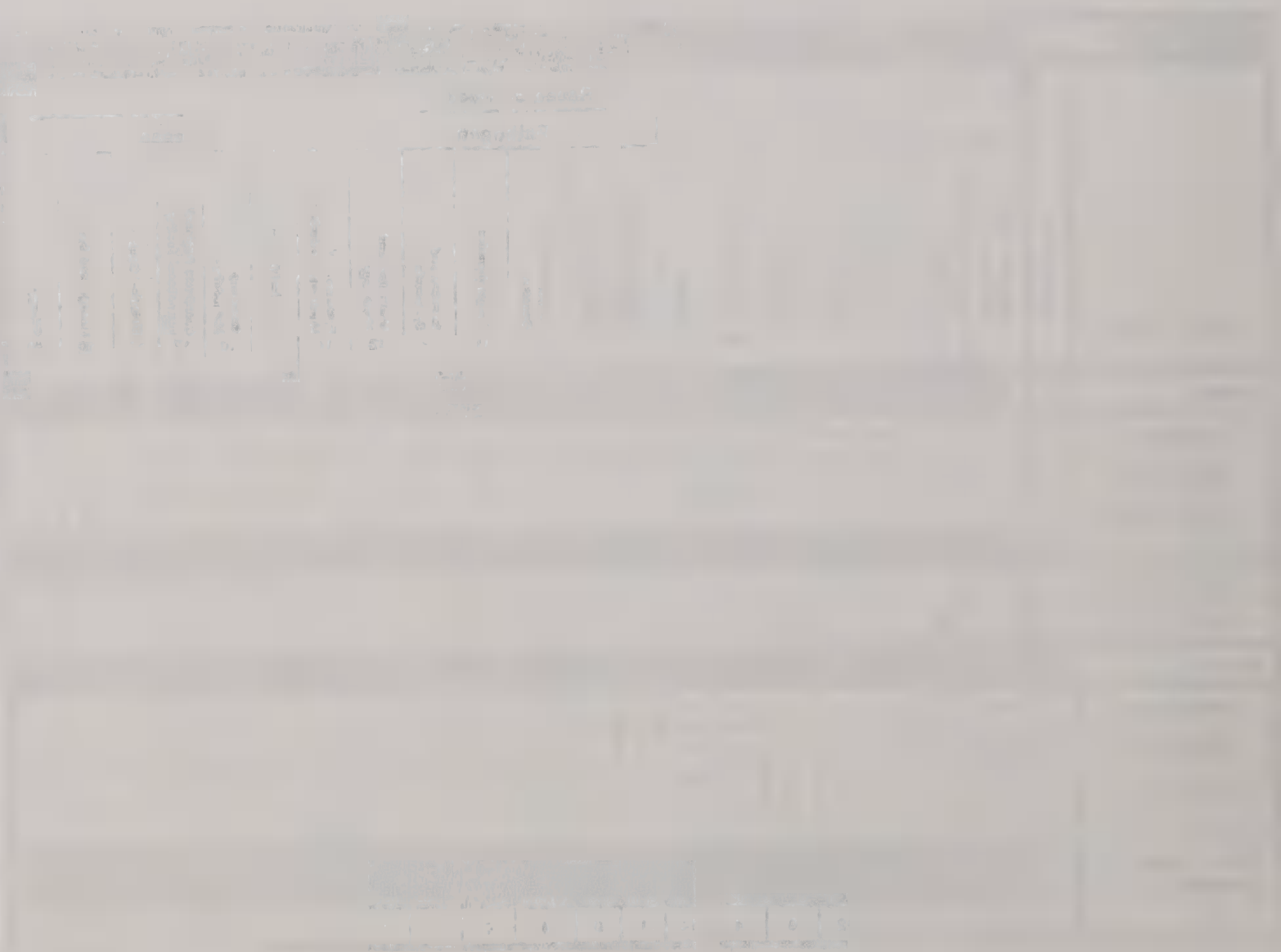
GROUP NEEDS ASSESSMENT

Application of the nominal group technique allowed each participant to vote for (in rank order) their top four priority research needs for each disease/host combination. Priority 1 received a score of 4, Priority 2 received a score of 3, etc. Several factors must be considered when interpreting the results (presented in the table which follows). These factors are:

- Each host/disease combination should be considered separately
- Each of the 20 "research needs" represents a grouping of more specific needs (see pages 5-7).
- Groupings of related "research needs," e.g., Mechanisms of Resistance and Genome Manipulation or Fungal Population Genetics and Fungal Genetics must be taken into consideration.

CEREAL RUST RESEARCH PRIORITIES

Disease Problem	PRIORITY	Research Needs																			
		Host							Pathogen						Disease						
		Germplasm Acquisition and Evaluation 1	Germplasm Enhancement 2	Gene Mapping 3	Cytology/Wide Crossing 4	Mechanisms of Resistance 5	Genome Manipulation 6	Genetics 7	Genome Mapping/Manipulation 8	Develop and Maintain Pathogen Germplasm 9	Fungal Population Genetics 10	Fungal Genetics 11	Evolution and Systematics 12	Metabolism and Physiology 13	Epidemiology/ Monitoring/Production 14	Chemical Control 15	Screening Methodology 16	Coordinate Regional/ International Testing 17	Biological Control 18	Management Systems 19	Ecology 20
Wheat																					
Leaf Rust	1	20	51	18	12	13	9	16	2	5	14	5	5	0	42	0	2	0	1	5	0
Stem Rust	2	11	50	23	15	18	6	7	14	8	2	14	3	0	42	0	4	0	1	0	0
Stripe Rust	3	22	47	23	13	12	5	8	2	5	4	3	3	0	41	3	2	0	1	14	1
Oats																					
Crown Rust	1	36	41	18	10	14	11	17	3	3	12	5	0	0	35	0	2	0	0	6	0
Stem Rust	2	31	45	20	7	23	8	20	6	5	5	7	4	1	22	0	2	0	0	0	0
Barley																					
Stripe Rust	1	43	57	18	6	5	13	11	1	0	5	11	0	3	34	7	9	0	1	0	4
Stem Rust	2-3	49	58	19	4	8	17	12	4	1	9	4	0	0	40	0	4	0	1	0	0
Leaf Rust	2-3	44	57	22	4	12	11	17	0	2	11	5	6	0	36	0	0	0	1	0	0
Crown Rust	4	45	31	14	4	6	7	4	6	0	14	11	20	3	39	4	5	3	1	0	4
Other Fungal Diseases																					
Scab		61	49	9	12	9	4	14	1	0	4	0	0	1	23	2	14	3	0	5	9



CURRENT RESEARCH INVENTORY

Cereal rust research is conducted at eight ARS locations (St. Paul, MN; Griffin, GA; Pullman, WA; Manhattan,KS; Fargo, ND; Ames, IA; Raleigh, NC; and Aberdeen, ID). Representatives of each location determined current research activity for each disease problem/research need combination. This inventory is presented in the following table.

CEREAL RUST RESEARCH LOCATIONS

Disease Problem	PRIORITY	Research Needs: Host							Pathogen						Disease						
		Germplasm Acquisition and Evaluation 1	Germplasm Enhancement 2	Gene Mapping 3	Cytology/Wide Crossing 4	Mechanisms of Resistance 5	Genome Manipulation 6	Genetics 7	Genome Mapping/Manipulation 8	Develop and Maintain Pathogen Germplasm 9	Fungal Population Genetics 10	Fungal Genetics 11	Evolution and Systematics 12	Metabolism and Physiology 13	Epidemiology/ Monitoring/Production 14	Chemical Control 15	Screening Methodology 16	Coordinate Regional/ International Testing 17	Biological Control 18	Management Systems 19	Ecology 20
Wheat																					
Leaf Rust	1	S,G,F, P,M,R, Ab	S,G, P,R, M	P,M	S,G, P,M, R	S,G, P,M	P	S,G P,M		S,M	S,G,P		S		S,G, M,R	R,M	R,M	S		R,M	M
Stem Rust	2	S,G,F. P,M	S,G, F,P, M	S,F P	S,P,F	S,F,P	P,F	S,F P	S	S,F, M	S,G,P	S,F	S	S	S,G, F,M	M	M,F	S		M	M
Stripe Rust	3	P,Ab	P,M	P	P	P	P	P		S,P	P	P	S,P		G,P	P	P	P		P	P
Oats																					
Crown Rust	1	S,G,R, Ab	S,G, R,A, Ab	S,A, Ab	A,R	S,A	S,A	A		S,A	S,G		S		S,G		S,R	S			
Stem Rust	2	S	S			S	S	S		S					S,G						
Barley																					
Stripe Rust	1	Ab	Ab	A							P				G,P	P					
Stem Rust	2-3	S,F,Ab	S,F	F		F		F		S,F		F			S,G, F		S,F	F			
Leaf Rust	2-3	R,Ab	R	A											G						
Crown Rust	4	Ab		A											G						
Other Fungal Diseases																					
Scab		S	S												G						

S= St. Paul, G=Griffin, P=Pullman, M=Manhattan, F=Fargo, R=Raleigh, A=Ames, Ab=Aberdeen

SUMMARY

A summary discussion revealed some hard truths, some contradictions, and a great deal of consensus. The workshop will prove especially beneficial as future decisions are made regarding cereal rust research funding, staffing, and research directions. Some important summary observations include:

- Cereal rust problems seem to be increasing at a time when available ARS resources will support fewer scientists.

- University support for cereal rust research is diminishing rapidly.

- Long-term strategies should be designed to give relatively timely and useful results.

- Applied programs must not be abandoned.

- Priorities from the workshop undervalued the importance of emerging technologies.

- Stripe rust of barley is a serious problem which is difficult to address at the Cereal Rust Laboratory (due to environmental constraints).

- Scab is a serious emerging problem. The most logical ARS location for an expanded effort is St. Paul.

- An unresolved question which needs to be addressed is whether it is a better use of available resources to characterize more genes "less well" or fewer genes "very well."

The workshop indicated that current resources are largely focused on the highest priority problems. Some gaps do exist, however, and some important research areas are being supported at such marginal levels as to cast doubt that they can be sustained. Industry support and awareness continues to be a critical component of this important research thrust.

ARS

RESEARCH PROJECT

SUMMARIES

AFS

RESEARCH PROJECT

SUMMARIES

ARS Cereal Rust Workers Workshop
Summary

Name: Donald V. McVey
Management Unit: Plant Protection Research
Location: St. Paul, MN
Strategic Unit Code: 2.2.1.1. 2.2.1.2

Project Title: Resistance factors for protection of wheat from stem and leaf rust and oats from crown rust.

Objectives/ Approach

The objectives of this research are the control of wheat stem and leaf rust and oat crown rust disease of their respective hosts.

Maintain the present level of stem rust protection in the Minnesota hard red spring wheat program and widen the protection against leaf rust. Continue cooperation with Nebraska breeders in developing stem rust resistant cultivars and broaden leaf rust resistance in their hard red winter wheat program. Recently, the winter wheat breeder of South Dakota has requested the same association as given to the Nebraska program. Assistance is being given to the South Dakota hard red spring wheat program and other programs. Entries of the USDA-ARS Wheat Small Grain Collection are being evaluated for their reaction to stem rust.

Develop hard red spring and winter wheat germplasm resistant to leaf and stem rust, using material primarily from Minnesota and Nebraska programs. Regional performance nurseries (Northern and Southern Hard Red Winter Wheat, Eastern and Southern Soft Red Winter Wheat, Hard Red Spring Wheat, and Durum) are monitored for their resistance level by testing with selected rust isolates in the seedling stage. They are also tested in the field with an artificially created epidemic using multiple rust races.

Genotypes of spring oats are being field evaluated for their reaction to crown rust. This included entries of the USDA-ARS Small Grain Collection, regional zone maturity nurseries and for adult plant resistance of the advanced U. of MN. breeding nursery. Artificial crown rust epidemic is created using multiple races of crown rust.

In cooperation with R. Busch and L. Szabo, identify RAPD markers linked to selected Sr genes. Also, I have been recently assigned the responsibility of overseeing the evaluation of wheat stem rust survey collections.

Summary

Name: William R. Bushnell

Management Unit: Cereal Rust Research

Location: St. Paul, MN

Strategic Plan Code: 2.1.2.1
2.2.1.2

Project Title: Gene expression and cytoplasmic events in resistance of cereals to rusts and powdery mildews

Objectives / Approach:

Objectives are twofold:

1) **To determine what host response genes contribute to expression of resistance in rust and powdery mildew diseases of cereals.**

2) **To develop new kinds of resistance genes based on use of genes for antifungal substances coupled to infection site-specific promoters, i.e. promoters of genes that are activated at sites of attempted penetration by rust and powdery mildew pathogens.**

Towards these objectives, host response genes are being isolated from oat inoculated with stem rust or powdery mildew, using differential screening of cDNA libraries. The relative amount, time, and localization of response gene transcripts are being determined in infected oat and barley using Northern blot analyses and *in situ* hybridization techniques. Methods are being developed to evaluate the role of individual response genes either by introducing the genes into oat using microprojectile bombardment of tissue cultures for selection and regeneration of stably transformed plants (in cooperation with D. Somers, Univ. of Minn.) or by transient expression in bombarded epidermal tissues. The timing and importance of response genes are also being evaluated using inhibitors of DNA synthesis and inhibitors of enzymes in the phenylpropanoid pathway.

Status of Research:

Expression of several response genes in barley was shown to increase within the first 4-8 hr after inoculation in powdery mildew of barley in both resistant and susceptible isolines. Use of cordycepin, an inhibitor of mDNA synthesis, indicated that gene transcription in the first 4-8 hr after inoculation is essential for expression of the hypersensitive response (HR) at 20-24 hr. OHPAS, an inhibitor of CAD (an enzyme in the phenylpropanoid pathway leading to lignin synthesis) strongly inhibited HR, implicating immediate precursors of lignin in resistance. Screening of cDNA libraries for response genes in oats is now underway. Two genes each for chitinase and glucanase have been introduced into oat tissue cultivars and are now in the selection/regeneration process. By using genes for anthocyanin production as markers, we can identify living, transformed epidermal cells for challenge with the powdery mildew fungus. Using this method, we will try to evaluate the role of individual response genes by introducing them along with the anthocyanin genes and then challenging transiently transformed cells with powdery mildew.

ARS Cereal Rust Workshop

Summary

Name: Kurt J. Leonard

Management Unit: Cereal Rust Laboratory

Location: St. Paul, MN

Strategic Plan Code: 2.2.1.1

Project Title: Durability of Rust Resistance and Population Genetics of Cereal Rust Fungi

Objectives/Approach:

Analyze virulence phenotypes in *Puccinia coronata* populations on cultivated oat in the U.S and wild oat in Israel in relation to epidemiology and pathogen fitness. Most genes for crown rust resistance in U.S. oat are from *Avena sterilis* from the Middle East. Levels of virulence in Israel indicate how these genes function in the naturally co-evolved system.

Test effects of uredinial infection density on competitive interactions of rust races on host plants. Little is known of competitive interactions between rust strains or how the competition affects overall population fitness of pathogens.

Model host-parasite co-evolution in gene-for-gene interactions. Environmental patchiness, gene flow, and population densities affect stability of polymorphisms for host resistance and pathogen virulence. Understanding the most important factors will improve agricultural use of race-specific resistace.

Characterize adult plant resistance in oat lines that have exhibited durable field resistance against crown rust in field nurseries near buckthorn.

Status of the Research:

Crown rust resistance genes collected in Israel in the 1960's still provide resistance to part of the *P. coronata* population, although virulence is more frequent in Israel than in the U.S. Significantly, virulence seems not to become fixed in wild pathogen populations as it does in agricultural systems.

We are studying effects of competition in mixed infections of spore color mutants of *P. graminis* f. sp. *tritici*. The isolates differ in infection efficiency and in the maximum numbers of uredinia that they can produce on wheat seedling leaves. We developed a mathematical model to distinguish effects of crowding from those of inter-strain competition.

Simulations with a host-pathogen co-evolution model show that polymorphisms of resistance and virulence are most likely to be maintained if there is a fitness cost of unnecessary virulence on susceptible host plants. When this is true, it is not necessary to have a fitness cost of resistance to maintain polymorphisms in the model. A low rate of gene exchange between pathogen populations markedly increases stability of polymorphisms in the model.

Nine oat lines developed at the University of Minnesota showed consistent field resistance to crown rust over 20 years in the buckthorn nursery. Most of these lines are susceptible as seedlings to all crown rust isolates we have tested. In field plots, seven lines exhibited substantially better resistance than cultivar Portage, which is a standard for slow rusting resistance.

Name: David L. Long

Location: St. Paul, MN

ARS Cereal Rust Workshop

Summary

Project Title: Durability of Rust Resistance and Population Genetics of Cereal Rust Fungi

Objectives/Approach:

Monitor and characterize the variation in virulence in Puccinia recondita in the U.S. annually. Race-specific resistance currently provides the most effective control of rust diseases of small grains. To maintain this resistance, changes in virulence in the rust fungi must be predicted or recognized before they cause excessive damage so that they can be countered with new combinations of reistance genes.

Determine the effects of resistances on cereal rust epidemic development. Rust epidemics in small grain crops can spread rapidly from southern U.S. to Canada, but development of epidemics is difficult to predict. Changes in cultural practices and regions where winter small grain crops are grown appear to have altered the pattern of rust epidemics.

Annually monitor progress of the individual rust diseases, and to predict the potential for epidemics and yield loss.

Status of Research:

In the past two years 1,000 collections were characterized and 82 virulence/avirulence phenotypes were found among 1462 single uredinial isolates on 14 host lines that are isogenic for leaf rust resistance. Regional race distribution patterns suggested that the central U.S. is a single epidemiological unit distinct from the eastern U.S. The distinctive racial composition of collections from the Southeast, Northeast and Ohio Valley indicate that populations of P. recondita in those area are discrete, suggesting epidemics originate from localized overwintering sources. Although collections from nurseries were not significantly more diverse than collections from fields, they did differ substantially in some areas.

In 1993 research information was transferred through the Cereal Rust Bulletin (9 issues) during the crop growing year, which summarized rust survey results, virulence identifications and epidemic progress.

In cooperation with plant breeders leaf rust resistance was identified in 344 cultivars and advanced breeding lines in 1993.

In 1993 the annual rust loss in the U.S. to wheat leaf rust rust was 88 million bushels or 4.8% of the crop.

Name: John J. Roberts
Management Unit: Plant Genetic Resources Conservation Unit
Location: Griffin, GA
Strategic Plan Code: 2.2.1.2
Project Title: Reducing Rust-induced Losses to Small Grains

Objectives/Approach: The major objective is to conduct research and development which will contribute knowledge and products to reduce losses suffered by small grains due to cereal rusts. Major approaches include: 1.) Conducting annual cereal rust surveys and epidemiological research, specializing in overwintering and oversummering phases, 2.) Conducting pathological, cytogenetic and genetic research on resistance of small grains to rusts and 3.) Developing rust-resistant small grain germplasm with particular emphasis on the needs of the Southeast. Specific areas of research are selected to augment programs of the Cereal Rust Laboratory and utilize expertise available at the host institution.

Status of Research: 1.) Cereal rust trap plots spaced along 1700 miles of Southeast highways provide samples from several environments important to cereal rust epidemic development. Data from these plots complement the annual, conventional rust surveys and provide data on other cereal pests. The speed with which rust detection data can be acquired with this system makes it a valuable tool to provide timely information for rust epidemic forecasting. With little modification, the technique can provide early season reports of cereal rust incidence and virulences.

2.) Wheat leaf epicuticular wax components are utilized by leaf rust sporelings with differential efficiency, ranging from a measured 5% to 95% transfer of ^{14}C fatty acids to $^{14}CO_2$. This utilization may extend the range of growth of the germ tubes, thus improving their chance to reach a stomate and successfully infect. Cultivars, existing or developed, having non-favored wax components, could reduce rust infection by limiting germ tube growth. Utilization can also be inhibited chemically, leading to the possibility of developing fungicides to do the same thing. Blocking this ability with PCMBS resulted in a 27% reduction in infection. Portions of this research have been patented and are being offered to industry through technology transfer channels. Additional pest resistance research has shown that leaf hairs often disrupt growth of leaf rust germ tubes, enough to reduce infection. Some disruption occurs when leaf hairs trap spores above the surface and either slow germination or force germ tubes to grow much farther than normal before finding a stomate. Other effects include blocking growing germ tubes and frequent instances of germ tubes coiling around the base of a trichome and not reaching a stomate. Elemental analyses using scanning electron microscope technologies revealed several potentially important differences in concentration of elements in both germ tubes and leaf hairs. High levels of calcium are present at the base of wheat leaf trichomes. Research has shown calcium to be involved in growth-altering response. Similar action may occur on the leaf surface when the germ tube encounters high concentrations of calcium.

3.) Six rust resistant soft wheat germplasm lines, Ceruga 1-6, have been released jointly by the USDA-ARS and the Georgia Agricultural Experiment Station. These lines are being used by breeders in the Southeast and feature effective new sources of rust resistance. Twelve more lines are candidates for germplasm release pending final field evaluations.

Summary

Name: Les J. Szabo
Management Unit: Cereal Rust Research
Location: St. Paul, MN
Strategic Plan Code: 2.2.1.1
2.2.1.2

Project Title: Molecular Genetic Mapping of Race-Specific Avirulence Genes in Cereal Rusts

Objectives / Approach:

The long-term objective of this program is to determine the biochemical and molecular genetic basis of race-specific resistance in cereal rust fungi. The short term objectives are: 1) develop the molecular genetic tools necessary to clone genes from rust fungi (genetic and physical maps, transformation system); 2) map and clone selected avirulence genes; 3) investigate the relative genome size and chromosome number of selected rusts; 4) investigate population genetics and phylogenetic relationships of rust fungi.

The first phase of this program was to investigate the physical structure of several cereal rust fungi to determine which species would be most amenable for molecular genetic study. Relative genome size is being determined from fluorescence of propidium iodide-stained nuclei as measured with a microscope photometer or flow cytometer and DNA reassociation kinetics. Chromosome numbers are determined from reconstructions of electron micrographs of serially sectioned pachytene nuclei. Molecular markers (RAPDs, STS and RFLPs) are being used to construct genetic maps of selected cereal rust fungi and map location of several avirulence genes. Map-based cloning will then be used to isolate these avirulence genes for molecular characterization.

Status of Research:

Chromosome number was determined to be 17 for *Puccinia coronata*, 18 for *P. graminis* f.sp *tritici*, and 18 for *Melampsora lini*. Currently, chromosome number is being determined for diverse isolates of *P. recondita*. Relative genome size was determined by for 14 rust species. *P. graminis*, *P. coronata*, and *P. sorghi* were in a group with the smallest genomes, about half the size of genomes in *P. hordei* and *P. recondita*. As a result of these findings, *P. graminis* f.sp. *tritici* has been selected as a model system for further molecular genetic studies. Reassociation kinetics was used to estimate genome size of *P. graminis* f.sp. *tritici* to be 67 million base pairs, of which 64% is comprised of single copy sequences and 34% moderately repetitive sequences. A genetic mapping population of *P. graminis* f.sp. *tritici* has been constructed, in which 15 different avirulence phenotypes are segregating. This mapping population is currently being used to construct a genetic map with RAPD markers. In addition, RAPD markers are currently being used to study population genetics of the North American asexual population of *P. graminis* f.sp. *tritici*. Several genes from *P. graminis* f.sp. *tritici* have been cloned and characterized and include a sporulation-specific gene (*usp*), and genes for glyceraldehyde 3-phosphate dehydrogenase and heat shock protein 70. Phylogenetic relationships of several cereal and grass rust fungi have been examined using DNA sequence data from the nuclear ribosomal RNA genes.

ARS Cereal Rust Workshop

Summary

Name: Steven Leath

Management Unit: Plant Science Research

Location: Raleigh, NC

Strategic Plan Code: 2,4.04.1.g
2,4.02.1.g

Project Title: Genetics of Disease Resistance, Epidemiology, and Control of Fungal Foliar Pathogens of Small Grains

Objectives / Approach:

To determine the epidemiology and yield reducing effects of powdery mildew and leaf rust of wheat in the Southeast; to determine the genetic basis of powdery mildew-wheat interactions including identification of resistance genes and determination of virulence gene frequency in *Blumeria graminis* f. sp. *tritici* populations; to introgress powdery mildew and Septoria leaf and glume blotch resistance from wild relatives into hexaploid wheat; to develop disease control decision guides for IPM use in wheat; to develop a simulation model for wheat growth and epidemic development for southeastern conditions. Genetic studies involve characterized isolates and pure genetic material in controlled conditions and disease and yield assessment studies, as well as population genetic studies, are completed in the field with endemic pathogen populations. Virulence analyses rely on differential lines with both direct inoculation with conidia and indirectly from ascospores, and in spore traps. Introgression work involves both interspecific and intergeneric crosses and embryo rescue onto tissue culture media. Quantification of somaclonal variation for agronomic and disease resistance traits, both between and within calli of soft red winter wheat cultivars is in progress. A decision guide programmed in C-language is now in testing to aid growers in making decisions with regard to controlling fungal foliar diseases of wheat.

Status of Research:

The role of powdery mildew in reducing wheat yields and the relationship between crop growth stage, disease levels and subsequent yield reduction has been detailed; the combined effects of leaf rust and powdery mildew on wheat development and yield are mostly detailed. Both deterministic and simulation models relating these factors are being developed. The virulence characteristics of *B. g.* f. sp. *tritici* populations in North Carolina have been determined and are being updated and the study expanded to a regional basis. Major soft red wheat cultivars are being analyzed to determine which, if any, powdery mildew resistance genes they carry. Determination of critical virulence thresholds that can be associated with subsequent epidemics on cultivars with specific resistance genes are in progress. Plants in the BC_1F_2 and BC_2F_2 generations have resulted from introgression of powdery mildew and glume blotch resistance from wild relatives (*Triticum monococcum, Aegilops squarrosa,* and *T. araraticum*) into hexaploid wheat via embryo rescue techniques. Crosses and molecular markers are now being used to evaluate their uniqueness. Somaclonal variation arising from between and within calli of soft red winter wheat cultivars is being quantified and toxin selected calli also are being evaluated for glume blotch resistance under field conditions. The USDA-ARS International Winter Wheat Powdery Mildew Program continues as a substantial portion of this project. In addition, germplasm enhancement and cooperative cultivar development efforts, as well as numerous other studies, also continue and joint germplasm and cultivar releases are now in progress.

ARS Cereal Rust Research Workshop

Name: Darrell M. Wesenberg

Management Unit: Small Grains and Potato Germplasm Research

Location: Aberdeen, Idaho

Strategic Plan Code: 2.1.2.5 Plant Germplasm Evaluation
2.1.1.4 Plant Germplasm Characterization

Project Title: Conduct & Coordination of Small Grains Germplasm Enhancement and Evaluation;
Small Grains Germplasm Evaluation

Objectives/Approach:

Relative to the ARS Cereal Rust Research Workshop, the project focus is on the evaluation and enhancement of barley germplasm for reaction to barley stripe rust race 24, primarily employing traditional evaluation and plant breeding approaches. The USDA-ARS National Small Grains Collection (NSGC) includes over 27,000 Hordeum accessions. The systematic evaluation of barley accessions in the NSGC and other elite germplasm is coordinated by ARS staff at Aberdeen. A cooperative barley germplasm evaluation effort concerned with stripe rust race 24 was initiated in 1990 in cooperation with Dr. William M. Brown, Jr., Vidal Velasco, and Dr. Joseph P. Hill, Colorado State University, Ft. Collins, Colorado under the terms of a Specific Cooperative Agreement between Colorado State University and ARS, with primary field evaluations in Bolivia.

Status of Research:

The 1993-94 Barley Stripe Rust Evaluation Nursery in Cochabamba, Bolivia included four groups: Group I composed of 669 previously tested barleys, largely NSGC accessions and varieties or advanced selections with putative resistance to barley stripe rust race 24; Group II composed of 2,189 elite barleys from Adolph Coors, Anheuser-Busch, ARS, Montana State Univ., North Dakota State Univ., Oregon State Univ., Plant Breeders 1, Univ. of California-Davis, Utah State Univ., Washington State Univ., and Western Plant Breeders; Group III composed of 2,968 previously untested NSGC accessions; and Group IV composed of 'Crystal' barley plants. Several NSGC accessions and other elite barley germplasm have been identified with putative resistance to barley stripe rust race 24 in one or more years of testing. A number of varieties grown commercially in the United States appear to be susceptible to race 24. The GRIN system currently includes stripe rust data from Cochabamba, Bolivia for 14,175 NSGC barley accessions. Barley stripe rust was first observed at the Aberdeen Research and Extension Center on July 29, 1993. Significant barley stripe rust infections occurred late in the season at Aberdeen, but the disease had little apparent influence on yield and grain quality. Progeny from crosses involving barleys with reported resistance to stripe rust race 24 were initiated at Aberdeen in 1990. Selections from these crosses have been evaluated for stripe rust race 24 reaction at Cochabamba, Bolivia and other locations where race 24 naturally occurs.

ARS Cereal Rust Workshop

Summary

Name: Roger P. Wise

Management Unit: Field Crops Research

Location: Ames, IA

Strategic Plan Code: 2.1.2.1
2.2.1.2

Project Title: Genetics of Host Resistance to Fungal Pathogens in Cereals

Objectives / Approach:

There are two interrelated goals of our research in the next five years. Identification of molecular genetic markers linked to genes for race specific resistance to crown rust (*Puccinia coronata*) in oats and powdery mildew (*Erysiphe graminis* f. sp. *hordei*) in barley, will be used for marker assisted selection in breeding programs and map-based cloning of resistance genes. Identification of syntenic groups linked to these resistance genes in oats, barley, rice, and wheat will facilitate broad base characterization of resistance to obligate fungal biotrophs.

Status of Research:

Resistance to oat crown rust:

Recently, efforts were begun to develop genetic maps of diploid and hexaploid oats based on morphological, RFLP, or RAPD-based markers. Our group has furthered the usefulness of these maps by positioning genes for resistance to crown rust, the most important fungal pathogen of oats. We have identified a cluster of genes for resistance in diploid oat and three regions for resistance in hexaploid oat. Until we initiated this project, the genetic organization of resistance to crown rust in the oat genome was virtually unknown. These markers will be used directly in oat breeding programs and will serve as focal points for experiments leading to the molecular isolation of oat genes. High resolution analysis of selected regions in diploid and hexaploid oat and the determination of homoeologous groups among these regions in barley, wheat, and rice are in progress.

Race specific resistance to Erysiphe graminis conditioned by the Mla complex in barley:

We have been developing a research program to investigate the genetics and molecular biology of resistance to *Erysiphe graminis* in barley, a model system for investigating specific recognition in gene-for-gene interactions among small grains and obligate fungal pathogens. The *Mla* locus is of particular interest because of its highly variable, multicomponent nature. It is located near the end of chromosome 5S, homeologous group 1 of the family *Gramineae*. Closely flanked by the endosperm storage protein genes, *Hor1* and *Hor2*, this locus has up to thirty dominant or co-dominant 'alleles' identified in different cultivars. We have developed a high resolution mapping population and have used this population to construct a high density RFLP map around the *Mla* locus. This is significant because the development of a high resolution, high density genetic map of the *Hor1/Mla/Hor2* region will be the foundation for a map based cloning strategy. The molecular isolation of race-specific resistance genes will enable a understanding of how they function ultimately leading to improved cultivars, aiding in integrated breeding programs and better control practices.

ARS Cereal Rust Workshop
May 24-25, 1994
Summary

Name: Stan Cox
Mgmt. Unit: Plant Science and Entomology Research Unit
Location: Manhattan, KS

Strategic plan code: 2.1.2.5
2.2.2.3

Project Title: Development of Hard Winter Wheat Germplasm with Multiple Pest Resistance

Objectives/Approach with Regard to Leaf Rust:

The wheat crop of the southern Great Plains has suffered staggering losses from infection by leaf rust for many years. Genetic resistance, the only form of protection currently feasible for farmers, will be provided in coming years by (1) adapted germplasm exhibiting "delayed susceptibility" of unknown genetic basis, (2) the few combinations of named *Lr* genes still effective in the region, and (3) new *Lr* genes transferred from other wild and cultivated species.

One of the objectives of this project is to develop a diverse array of leaf-rust resistant germplasms with high productivity and quality under Great Plains conditions. The sources of resistance genes used are the diploid and tetraploid progenitors of common wheat, including *Triticum tauschii, T. monococcum, T. boeoticum, T. urartu, T. araraticum,* and *T. turgidum*. The approach employed is to exploit intraspecific diversity by crossing a relatively large number of accessions of each species directly with elite winter wheat cultivars or breeding lines, to limit segregation to one genome (two for tetraploid sources), to field test both resistant and susceptible BC_1- or BC_2-derived lines at the earliest stage possible, and to expose populations to a wide range of growing conditions.

A corollary objective is to determine the locations, inheritance, and phenotypic effects of introgressed resistance genes and other important genes transferred along with them. Approaches include allelism studies, aneuploid analyses, and linkage studies using molecular markers.

Status of Research:

Germplasms released since 1990 include KS90WGRC10 (*Lr41, T. tauschii* source, seedling, 1D), KS90WGRC11 (*Lr42, T. tauschii*, seedling, 1D), KS90WGRC12 (*T. tauschii,* adult-plant gene(s)), KS92WGRC15(*Lr21*), KS92WGRC16 (*Lr43, T. tauschii*, seedling, 7D), and KS92WGRC23 (*T. monococcum* source, seedling). In field trials over eight locations in up to three years, BC_2-derived lines carrying *Lr41* or *Lr42* had up to double the grain yield and over one percentage point higher grain protein than their recurrent parents under leaf-rust infection. In absence of leaf rust, the lines and recurrent parents had equal yield and grain protein.

Several newly developed lines with resistances from *T. monococcum, T. boeoticum,* and *T. araraticum* are now undergoing genetic studies and field-testing. The gene from *T. boeoticum* carried by one of these lines shows linkage to three RFLP loci that map to homoeologous group-2 chromosomes. Lines carrying resistance genes from two *T. monococcum* accessions are being studied histologically to determine whether they express prehaustorial leaf-rust resistance, a form of resistance that could prove to be more durable than hypersensitivity. Transfer of genes from *T. monococcum* into hard winter wheats is usually blocked by inviable or totally sterile F_1 hybrids. We have found RAPD markers that are linked to a gene allowing formation of female-fertile hybrids between hexaploid wheats and *T. monococcum*.

ARS Cereal Rust Workshop

Name: Merle G. Eversmeyer

Management Unit: Plant Science and Entomology Research

Location: Manhattan, Kansas

Strategic Plan Code: 2.1.2.5
2.2.2.3

Project Title: Epidemiology and Ecology of Wheat Rusts in the Central Great Plains

Objectives/Approach:

Epidemics of wheat leaf rust alone have caused a 5.7% annual reduction in 1984-1993 wheat production in the Central Great Plains of the US. Loss estimates for 1992 and 1993 KS wheat production averaged 11%. Producers planting wheat cultivars without resistance to the prevailing pathogens have increased the risk of major yield losses in the last decade. The primary objectives are the development of multiple control strategies of pest resistance for wheat. The interrelated objectives and approaches are: 1. Improve methods for wheat leaf rust control, which emphasize host plant resistance, host:parasite interactions and population dynamics by searching germplasm sources to which the pathogen population is avirulent; and 2. To determine the ecology and epidemiology of wheat diseases and their interactions to develop pest control strategies by determining the biometeorological interrelationships operative in epidemic development and resulting losses in multiple disease epidemics. Develop models of multiple disease epidemics based on available biometeorological data.

Status of research:

Steady progress is being made in the incorporation of leaf rust resistance into germplasm in the Great Plains. The World Wheat Collection has been screened against a composite of pathogen virulences (1,2,3,9,10,11,15,17,18,24) found in the Great Plains.

Survival of airborne Puccinia recondita and P. graminis urediniospores was reduced to less than 5% within 24 hrs of exposure to subfreezing temperatures and 0% within 96 hrs. P. recondita and P. graminis spores retained 50-80% germination after exposure for 120 hrs at temperatures from 10-35 and 20-35 C, respectively for 120 hrs.

Models of overwintering of leaf rust were developed for the Manhattan area by regressing levels of observed overwintering (0-9) observed on March 15th in nurseries against average daily max/min temperatures, precipitation, and snow cover and/or daily deviations from the 10-yr averages for each weather variable summed over a 10-day period prior to the date of prediction.

ARS Cereal Rust Workshop

Summary

Name: Robert Busch

Management Unit: Plant Science Unit

Location: St. Paul, MN

Strategic Plan Code: 2.1.2.5

Project Title: Wheat Genetics and Improvement

Objectives / Approach:

Partial goals of the project are to evaluate the genetic control and develop new sources of genetic diversity in spring wheat for useful traits in cooperation with other scientists. Included in this improvement are: (1) incorporation or selection of new sources of resistance to diseases in wheat (primarily--stem and leaf rust, scab, and leaf spotting); (2) germplasm diversity groups in North American spring wheat cultivars; and (3) release of germplasm to the public and coordination of the Uniform Regional Hard Spring Wheat Nursery.

Specifically, incorporation or selection of new sources of resistance to diseases will be discussed. Close cooperation with Dr. D. McVey (USDA-ARS, Cereal Rust Lab) is essential in the development of rust resistant spring wheat germplasm. New sources (such as Lr19) and/or combinations of potentially new resistances are produced by Dr. McVey, are often improved, and then given to the wheat program for incorporation with well adapted or newer selections of spring wheat. Inoculation of rust spreader rows for the early generation nurseries are routinely done each year by Dr. McVey. These inoculated nurseries are critical in the continued development of rust resistant cultivars and to maintain a high level of resistance in the breeding germplasm. Further, Dr. McVey has a rust (stem and leaf) nursery each year for preliminary yield trial lines, advanced yield trial lines, released cultivars, and the entries in the Uniform Regional Hard Red Spring Wheat Nursery and Durum Uniform Regional Nursery. Leaf rust resistance in the Minnesota program involves using the adult plant resistance (Lr13 and Lr34) with additional genes from numerous sources.

Status of Research:

The spring wheat germplasm in the north central region is evaluated on a yearly basis with multiple isolates of stem rust and common isolates of leaf rust. Difficulties have been encountered in following new genes incorporated into the germplasm since the level of resistance is quite high to both rust pathogens in the spring wheat region. Molecular approach have been initiated to detect certain major stem rust resistance genes in cooperation with Dr. Szabo. Resistance genes in alien species may begin to be incorporated as more knowledge is gained.

ARS Cereal Rust Workshop
Summary

Name: Roland F. Line

Management Unit: Wheat Genetics, Quality, Physiology and Disease Research

Location: Pullman, Washington

Strategic Plan Code: 2.2.1.2 and 2.2.1.3

Project Title: CONTROL OF FOLIAR DISEASES AND SMUTS OF WHEAT

Objectives/Approach: The overall objectives are to conduct basic and applied research on the control of foliar diseases and smuts of wheat, especially stripe rust, leaf rust, stem rust, and flag smut, and to coordinate research on cereal rusts and smuts in western United States, national research on stripe rust, and the international program on germplasm evaluation for stripe rust resistance. The objectives that will be emphasized for the next five years are 1) to determine epidemiological, morphological, cytological and genetical characteristics of resistance to stripe rust and leaf rust of wheat; identify and evaluate new germplasm and gene combinations for resistance; and develop improved methods of using diverse sources and combinations of resistance and 2) to develop and improve methods for predicting wheat diseases, assessing losses, and controlling cereal diseases, and utilize the information to develop an improved expert system for integrated management of wheat diseases (MoreCrop).

The approach emphasizes integrated control of wheat diseases, especially stripe, leaf, and stem rust. It consists of field, greenhouse, and laboratory research on determining epidemiological, morphological, cytological, and genetical characteristics of resistance; developing, improving, and utilizing methods for predicting epidemics; assessing losses caused by diseases; integrating resistance, chemicals, and crop management to control diseases; and developing and improving an expert system for managing wheat diseases in the West, expanding the system to other regions, improving educational use of the system, and integrating the system with other crop management systems.

Status of Research: Research on this project has resulted in major progress in controlling cereal rusts, especially in identifying critical factors that affect the diseases, understanding race evolution and distribution, predicting epidemics, understanding resistance, identifying resistance genes and determining their inheritance and chromosomal location, developing cultivars with durable resistance, developing procedures for using chemicals in an integrated disease control program, and developing an expert system for managing wheat diseases. Consequently, losses caused by rusts and smuts have been reduced and often prevented. Since 1980, integrated use of fungicides has prevented annual losses in Washington of 1,000,000 bu or more. Use of cultivars with durable resistance to rust has also prevented multimillion dollar losses. Most recently, we have determinated the inheritance of 41 different genes (29 not previously named) for seedling resistance to stripe rust, chromosomal location of 33 of the genes, inheritance of eight high-temperature, adult plant resistance genes, and relationship and evaluation of rust races based on virulence and RAPD analyses, and have developed and implemented an expert system for managing wheat diseases called MoreCrop (Managerial Options for Reasonable Economical Control of Rusts and Other Pathogens). Research on barley stripe rust has been initiated. A small percentage of the research is on control of common bunt, flag smut, and dwarf bunt.

ARS Cereal Rust Workshop
Summary
May 24-25, 1994

Name: Stephen Jones

Management Unit: Wheat Genetics, Quality, Physiology and Disease Research Unit

Location: Pullman, WA 99164-6420

Strategic Plan Code: 2.1.01.1.e (20%)
2.2.03.1.c (80%)

Project: Mapping stripe rust resistance genes to chromosomes (with R Line)

Objectives: Determine the chromosomal location of over 20 new or previously unmapped stripe rust resistance genes.

Status: Most of the race specific genes have been located to chromosomes. Determination of linkage relations and transfer of the most important genes will be initiated. Race nonspecific genes are also being mapped in monosomic derived advanced generations.

Project: Determining stripe rust resistances to PNW races in collections of *T. tauschii* (with TS Cox) and *Dasypyrum villosum* (with CO Qualset, UC Davis and Ciro DePace, Potenza, Italy).

Objectives: To evaluate very diverse populations for their disease resistance gene dynamics. Also gene donors will be identified which carry multiple resistances to PNW pathogens.

Status: The race specific work on *T. tauschii* is complete. The work on *D. villosum* is underway. Screening for resistance to eyespot and cephalosporium stripe is also under way. These lines are also being used to produce new amphploids which will be used in further genetic studies and transfers.

ARS Cereal Rust Workshop
Summary

Name: R. E. Allan
Management Unit: Wheat Genetics, Quality, Physiology and Disease Research
Location: Pullman, WA
Strategic Plan Code: 2.1.01.1.e (20%) 2.2.03.1.c (80%)
Project Title: Genetic Approaches in Wheat for Yield Stability, Enhanced Quality, and Reduced Vulnerability to Plants

Objectives/Approach: Combine durable resistances to stripe, leaf, stem rust and powdery mildew into wheat germplasm adapted to the Pacific Northwest. Develop germplasm for use in wheat multilines to simultaneously reduce vulnerability to rusts and powdery mildew. Move unique foliar disease resistance genes into compatible wheat genetic backgrounds. new resistance to each of the rusts and to powdery mildew are selected based on information provided by R. E. Allan and R. F. Line, or from regional and international cooperators. They are used as parents in crosses with adapted club and common soft white winter parents. Early generation lines are screened for resistance as seedlings to 2 or more biotypes of the stripe rust pathogen with diverse genes for virulence. Field tests in 3 to 5 environments conducive to foliar diseases are used to assess resistance to natural occurring epiphytitics of the rusts and powdery mildew. Inoculations using multiple stripe rust biotypes are made at the Pullman site. Cyclical breeding procedures are used to combine individual resistances possessed by promising early generation lines into well adapted-high-quality club and common soft white winter (SWW) wheat genetic backgrounds. Two different genetic male sterility systems transferred into adapted cvs. are used for the procedure. Candidates of multiline components are generated simultaneously. Main emphasis is on club wheats using high-quality adapted genotypes as parents, which have stripe rust adult-plant resistance (HTAPR).

Status of Research: A gene from *T. dicoccoides* that is resistant to all USA stripe rust biotypes was transferred to PNW germplasm. Germplasm putatively possessing this gene and 3 other race-specific genes and 1 nonspecific gene for resistance are in replicated tests. Many of our current advanced lines have the closely linked genes for resistance to stripe *(Yr17)*, leaf *(Lr37)* and stem rust *(Sr38)* reported to be on 2AS. Madsen and Hyak were bred by this project; both carry these 3 linked genes and the *Pch*1 gene for foot rot resistance. They were grown on over 1 million ac in the region in 1993. Rulo club wheat, will be released in 1993; it has these 3 rust genes plus 2 additional *Yr* genes and is heterogeneous for a *Pm* gene.

Advanced lines are in yield and quality tests that have unidentified genes for stripe rust and stem rust resistance derived from *Lophopyrum elongatum*. One line (PI561033) also has tolerance to strawbreaker foot rot and high resistance to cephalosporium stripe.

A new multiline (ARS 9423) comprised of components having several different genes for leaf rust and stripe rust resistance and 2 different genes for strawbreaker foot rot resistance, is in advanced yield tests.

Working in the hypothesis that partial resistance may be indicative of durable adult plant stripe rust resistance, we have selected 200 lines from a bulk blend of the ARS wheat collection. Lines lacking seedling resistance will be used as potentially new sources of HTAP resistance.

ARS Cereal Rust Workshop Summary

Name: James D. Miller

Management Unit: Cereal Crops Research

Location: Fargo, ND

Strategic Plan Code: 2.1.2.3
2.1.2.5

Project Title: Enhancement of Wheat Germplasm through Improved Pest Resistance, Quality and Agronomic Traits

Objectives/Approach:

Since the release of common and durum spring wheat cultivars having various combinations of multiple resistance genes or gene pyramiding, there has not been a serious epidemic of stem rust on wheat in the northern Great Plains.

However, because the stem rust fungus has the ability to change through mutation, sexual recombination and nuclear reassociation, it is necessary to continually monitor the rust population for new virulent pathotypes and search for new sources and types of resistance that can be used for incorporation and maintaining genetic resistance in the development of wheat cultivars.

Search for useful genetic resistance to stem rust within the alien species related to wheat and domestic wheats. Identify and transfer the desirable genes into tetraploid and hexaploid wheats for use in the improvement of the germplasm of cultivated wheats and determine the association of components of slow rusting resistance in winter wheat. Develop mutant and recombinant test cultures and methods for inducing genetic variability in the pathogen. Determine the chromosomal location of genes for resistance to a recombinant culture virulent on a previously widely grown resistant wheat.

Because of the gene for gene relationships between pathogen and host, use appropriate cultures and predict, without crossing, whether or not the resistance genes in an alien species are already present in cultivars, and use cytogenetic stocks and breeding procedures to incorporate the unknown useful genes into germplasm lines. Use mutagens and hybridization on the barberry plant to develop stem rust cultures that are useful in predicting new virulence, identifying useful genes in alien species, and simultaneous testing for the presence of two resistance genes in a single plant. Use breeding and cytogenetic procedures to determine the inheritance and chromosomal location of resistance genes.

Status of Research:

A sexual recombinant culture, 46-2, of the wheat stem rust fungus derived from random selfing and crossing on barberry plants was highly virulent in the previously resistant wheat cultivar Waldron, but avirulent in cultivars Len, Coteau, and Stoa. Tests in the third generation seedling from a diallel cross of the four cultivars confirmed that Len differs from Waldron by a dominant gene conditioning infecting type (IT) 2. Coteau and Stoa have a dominant gene conditioning IT 2 that is different from the one in Len. Both Coteau and Stoa differ from Waldron by an incompletely dominant gene conditioning IT 0;, when homozygous. Stoa may have a second gene conditioning IT 2, or a total of 3 genes for resistance. Certain plants of Coteau also have a dominant gene for thermosensitive resistance, showing resistance at 21°C and susceptibility at 27°C. The recombinant stem rust culture is very useful in predicting, without crossing, the presence or absence of genes for resistance, identifying resistance genes not detected by cultures previously available, predicting possibly future shifts in virulence, and detecting additional genes for resistance in a gene pyramiding breeding strategy. Research to map the genes from Len, Coteau, and Stoa on specific chromosomes is in progress.

The presence of at least 10 known *Sr* genes (*Sr7, 8, 9, 10, 11, 12, 15, 16, 17,* and *36*) or similar genes were postulated as being present in some of the 166 accessions of *Triticum dicoccoides* tested with 4 stem rust test cultures. Twelve accessions possess a combination of known genes along with unidentified genes for resistance which may be useful in widening the narrow 2 to 4 gene base for stem rust resistance in domestic durum wheats.

Information on methods for quickly and reliably detecting gene *Rpg1* in barley and resistance gene(s) to the new wheat stem rust pathotype, Pgt-QCC, virulent on barley cultivars possessing *Rpg1* is necessary in incorporating the new gene for resistance to QCC and retaining the old durable resistance *Rpg1* in barley cultivars. Identification has been difficult because many pathotypes produce a mixture of low and high infection type (IT) on seedling plants of lines possessing *Rpg1*. In contrast, distinct differences in IT were produced by Pgt-MCC and -HPH; genetically diverse lines with *Rpg1* showed low IT and effectively detected the *Rpg1* gene. Those lines with *rpg1* consistently exhibited intermediate or high ITs. With this reliable method, lines can now be tested for *Rpg1* or a similar gene within 20 days. Research to develop stem rust spore color mutants for simultaneous testing of a barley line for the presence of *Rpg1* and resistance gene to QCC is in progress.

Ninety-three domestic spring bread, durum and advanced lines of wheat were resistant to natural occurring stem rust. In an induced epidemic of five specific cultures, most wheats possessed adequate resistance genes; however, some bread wheats exhibited variable size pustules on the same plant and severity up to 20%. This level of protection is not adequate if the natural inoculum of these races increases. Analysis for probable genotype of these wheats is in progress.

ARS CEREAL RUST WORKSHOP SUMMARY

Name: Norman D. Williams

Management Unit: Cereal Crops Research

Location: Fargo, ND

Strategic Plan Code: 2.1.2.3
2.1.2.5

Project Title: Enhancement of Wheat Germplasm through Improved Pest Resistance, Quality, and Agronomic Traits

Objectives/Approach:

Develop genetic stocks of wheat and methods for genetic analysis and incorporation of genetic resistance to stem rust into durum and common wheat germplasm. Determine the inheritance and chromosomal location of genes for resistance. Search for sources of stem rust resistance and create new genetic variability in wheat and in the stem rust pathogen. Release enhanced germplasm.

Use breeding and cytogenetic procedures to develop genetic stocks in durum and common wheat and determine the inheritance of stem rust resistance and chromosomal location genes for resistance. Survey and evaluate alien species related to wheat for stem rust resistance and use cytogenetic stocks, mutants and breeding procedures to incorporate useful genes for resistance. Use mutagenic chemicals to induce mutations for stem rust resistance. Use hybridization and mutagens to develop stem rust strains useful in identifying new genes for resistance in wheat.

Status of Research:

A recombinant culture, 46-2, of the stem rust fungus derived from selfing and crossing on barberry plants was used to test seedlings from crosses of resistant bread wheat cultivars Len, Coteau, and Stoa with susceptible Waldron. Tests on third generation seedlings confirmed that Len has a dominant gene conditioning infection type 2. Coteau and Stoa have a gene different from the one in Len that conditions infection type 2. Both Coteau and Stoa have an incompletely dominant gene conditioning infection type (0;) when homozygous (true breeding). Stoa may have a second gene conditioning infection type 2, or a total of three genes for resistance. Some plants of Coteau also have a dominant gene for thermosensitive resistance, showing resistance at low temperature and susceptibility at high temperature. The recombinant stem rust culture is very useful in differentiating genes for resistance not detectable by cultures previously available. It can detect new genes added in a breeding scheme to pyramid or stack genes in new cultivars. Gene pyramiding provides a more permanent genetic barrier against the stem rust fungus. Research to map the genes from Len, Coteau, and Stoa on specific chromosomes is in progress.

The winter wheat cultivar, Triumph 64 (Tmp 64), is one of a standard international set of cultivars or lines used to differentiate races of stem rust on the basis of genes for virulence in the pathogen. We found that a spring wheat line with its resistance derived from Tmp 64 has two genes for resistance instead of the one gene proposed earlier by other scientists. Mapping of these genes to specific chromosomes is in progress.

A chemically induced multiploid mutant in durum shows promise for facilitating incorporation of alien genes without use of chromosome doubling agents. Chemically induced mutants of the suppressor gene on chromosome 7DL indicate that up to three or more genes for stem rust resistance in the cultivar Canthatch are being suppressed.

TITLE: Transfer of a gene for stem rust resistance from *T. speltoides* to durum.

AUTHOR: Leonard Joppa and J. D. Miller Location: Fargo, ND

PROBLEM: Stem rust of wheat has not been a problem in the Northern Great Plains for a number of years. Almost all cultivars that are released by both public and private breeders are carefully tested to assure that they have genetic resistance to the common cultures of stem rust. Occasionally, a private breeder has released a cultivar that lacks resistance, but they have paid a heavy price.

It is important that we do not become complacent about our success in controlling this disease, because it has been shown that new virulent races may emerge with little warning. Therefore, we have continued to search for new sources of resistance in alien species from the tribe Triticeae.

APPROACH: Accessions of a number of species were investigated for the presence of genes for rust resistance. *Triticum speltoides* has considerable diverse resistance to rust. Some of these genes have previously been transferred to wheat (Knott, Dvorak). One accession appeared to give immunity to all races or cultures against which it was tested. It was crossed with Langdon durum and a chromosome addition line that had the resistance was obtained. The addition line was crossed with Langdon 5D(5B) disomic substitution line to obtain a translocation.

RESULTS: After several years of crossing and selecting, we have a line that has a translocation, but the chromosome also has genes that prevent fertility when homozygous. That is, all plants homozygous for the translocated chromosome are male sterile (though female fertility appears normal). Crosses have been made with a rust susceptible line that also has the homoeologous pairing gene ph1b in an attempt to shorten the translocation and eliminate the sterility.

CONCLUSION: The study has resulted in the production of a rust susceptible durum wheat line (47-1). The homoeologous pairing gene produced by the late E. R. Sears has been transferred to this durum wheat line. This line should be useful in transferring genes to durum wheat from alien species.

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